FIG. 1A

```
1    CTGCTTCCCACCAGCAAAGACCACGACTGGAGAGCCGGAGCCAGCTGGAAACATG    60
     ------+---------+---------+---------+---------+---------+
     GACGAAGGGTGGTCGTTTCTGGTGCTGACCTCTCGGCCTCGTCGACCCTTTGTAC
                                                          M

61   AAGAGCGGTCTTGCTGCTGACCACGCTCCTCGTGCCTGCACACCTGGTGGCCGCCTGGAGC  120
     ------+---------+---------+---------+---------+---------+
     TTCTCGCCAGAACGACGACTGGTGCGAGGAGCACGGACGTGTGGACCACCGGCGGACCTCG
      K  S  V  L  L  L  T  T  L  L  V  P  A  H  L  V  A  A  W  S

121  AATAATTATGCGGTGGACTGCCCTCAACACTGTGACAGCAGTGAGTGCAAAAGCAGCCCG  180
     ------+---------+---------+---------+---------+---------+
     TTATTAATACGCCACCTGACGGGAGTTGTGACACTGTCGTCACTCACGTTTTCGTCGGGC
      N  N  Y  A  V  D  C  P  Q  H  C  D  S  S  E  C  K  S  S  P

181  CGCTGCAAGAGGACAGTGCTCGACGACTGTGGCTGCTGCCGAGTGTGCGCTGCAGGGGCGG  240
     ------+---------+---------+---------+---------+---------+
     GCGACGTTCTCCTGTCACGAGCTGCTGACACCGACGACGGCTCACACGCGACGTCCCGCC
      R  C  K  R  T  V  L  D  D  C  G  C  C  R  V  C  A  A  G  R
```

FIG. 1B

```
                                                              300
241  GGAGAAACTTGCTACCGCACAGTCTCAGGCATGGATGGCATGAAGTGTGGCCCGGGGCTG
     ----------+---------+---------+---------+---------+---------+
     CCTCTTTGAACGATGGCGTGTCAGAGTCCGTACCTACGTACTTCACACCGGGCCCCCGAC
     G  E  T  C  Y  R  T  V  S  G  M  D  G  M  K  C  G  P  G  L

                                                              360
301  AGGTGTCAGCCTTCTAATGGGAGGATCCCTTTGGGTGAAGAGTTTGGTATCTGCAAAGAC
     ----------+---------+---------+---------+---------+---------+
     TCCACAGTCGGAAGATTACCCCTCCTAGGGAAACCCACTTCTCAAACCATAGACGTTTCTG
     R  C  Q  P  S  N  G  E  D  P  F  G  E  E  F  G  I  C  K  D

                                                              420
361  TGTCCCTACGGCACCTTCGGGATGGATTGCAGAGAGACCTGCAACTGCCAGTCAGGCATC
     ----------+---------+---------+---------+---------+---------+
     ACAGGGATGCCGTGGAAGCCCTACCTAACGTCTCTCTGGACGTTGACGGTCAGTCCGTAG
     C  P  Y  G  T  F  G  M  D  C  R  E  T  C  N  C  Q  S  G  I

                                                              480
421  TGTGACAGGGGGACGGGGAAAATGCCTGAAATTCCCCTTCTTCCAATATTCAGTAACCAAG
     ----------+---------+---------+---------+---------+---------+
     ACACTGTCCCCCTGCCCCTTTTACGGACTTTAAGGGGAAGAAGGTTATAAGTCATTGGTTC
     C  D  R  G  T  G  K  C  L  K  F  P  F  F  F  Q  Y  S  V  T  K
```

FIG. 1C

```
481   TCTTCCAACAGATTTGTTCTCTCCACGGAGCATGACCATGGCATCTGGAGATGGCAATATT
      ------+---------+---------+---------+---------+---------+
      AGAAGGTTGTCTAAACAAAGAGAGTGCCTCGTACTGGTACCGTAGACCTCTACCGTTATAA  540
      S   S   N   R   F   V   S   L   T   E   H   D   M   A   S   G   D   G   N   I

541   GTGAGAGAAGAAGTTGTGAAAGAGAATGCTGCCGGGTCTCCCGTAATGAGGAAATGGTTA
      ------+---------+---------+---------+---------+---------+
      CACTCTCTTCTTCAACACTTTCTCTTACGACGGCCCAGAGGGCATTACTCCTTTACCAAT  600
      V   R   E   E   V   V   K   E   N   A   A   G   S   P   V   M   R   K   W   L

601   AATCCACGCTGATCCCGGCTGTGATTTCTGAGAGAAGGCTCTATTTCGTGAYTGTTCAA
      ------+---------+---------+---------+---------+---------+
      TTAGGTGCGACTAGGGCCGACACTAAAGACTCTCTTCCGAGATAAAGCACTRACAAGTT  660
      N   P   R   *

661   CACACAGCCAACATTTAGGAACTTCTAGATTATAGCATAAGGACACATGTAATTTTTGAA
      ------+---------+---------+---------+---------+---------+
      GTGTGTCGGTTGTAAATCCTTGAAAGATCTAATATCGTATTCCTGTACATTAAAAACTT  720

721   GACCAAAATGTGATGCATGGTGGATCCAGAAAACAAAAGTAGGATACTTACAATCCATAA
      ------+---------+---------+---------+---------+---------+
      CTGGTTTTACACTACGTACCACCTAGGTCTTTTGTTTTTCATCCTATGAATGTTAGGTATT  780
```

FIG. 1D

```
781  CATCCATATGACTGAACACTTGTATGTGTTTGTTAAATATTCGAATGCATGTAGATTGT
     ------+---------+---------+---------+---------+---------+  840
     GTAGGTATACTGACTTGTGAACATACACAAACAATTTATAAGCTTACGTACATCTAAACA

841  TAAATGTGTGTATAGTAACACTGAAGAACTAAAAAATGCAATTTAGGTAATCTTACATG
     ------+---------+---------+---------+---------+---------+  900
     ATTTACACACATATCATTGTGACTTCTTGATTTTTACGTTAAATCCATTAGAATGTAC

901  GAGACAGGTCAACCAAAGAGGGAGCTAGGCAAAGCTGAAGACCGCAGTGAGTCAAATTAG
     ------+---------+---------+---------+---------+---------+  960
     CTCTGTCCAGTTGGTTCTCCCTCGATCCGTTCGACTTCTGGGCGTCACTCAGTTTAATC

961  TTCTTTGACTTTGATGTACATTAATGTTGGGATATGGAATGAAGACTTAAGAGCAGGAGA
     ------+---------+---------+---------+---------+---------+  1020
     AAGAAACTGAAACTACATGTAATTACAACCCTATACCTTACTTCTGAATTCTCGTCCTCT

1021 AGATGGGGAGGGGGTGGGAGTGGGAAATAAAATATTAGCCCTTCCTTGGTAGGTAGCTT
     ------+---------+---------+---------+---------+---------+  1080
     TCTACCCCCTCCCCCACCCTCACCCTTTATTTATAAATCGGGAAGAACCATCCATCGAA
```

FIG. 1E

```
1081  CTCTAGAATTTAATTRTGCTTTTTTTTTTTTTTGGGCTTTGGGAAAAGTCAAAATAAA  1140
      ---------+---------+---------+---------+---------+---------+
      GAGATCTTAAATTAAYACGAAAAAAAAAAAAAAACCCGAAACCCTTTTCAGTTTTATTT

1141  ACAACCAGAAACCCCTGAAGGAGTAAGAGTGTTGAAGCTTATGGAAATTTGAGTAACA  1200
      ---------+---------+---------+---------+---------+---------+
      TGTTGGTCTTTGGGGACTTCCTTCATTCTCACAACTTCGAATACCTTTAAACTCATTGT

1201  AACAGCTTTGANCTGAGAGCAATTYCAAAGGCTGCTGATGTAGCCCCCGGGTTNCCTNT  1260
      ---------+---------+---------+---------+---------+---------+
      TTGTCGAAACTNGACTCTCGTTAARGTTTCCGACGACTAC:ATCGGGGGCCCAANGGANA

1261  NTCTNAAGGAC  1271
      ---------+-
      NAGANTTCCTG
```

FIG. 2

```
                1                                                    50
ce10_chick   ...MGSAGAR  P.ALAAALLC  LARLALGSPC  PAV....CQC  ...PAA.APQ
cyr6_mouse   ...MSSSTFR  TLAVAVTLAH  LTRLAL.STC  PAA....CHC  ...PLE.APK
ctgf_human   .MTAASMGPV  RVAFVVLLAL  CSRPAVGQNC  SGP....CRC  ...PDEPAPR
fisp-12      .MLASVAGPI  SLAL.VLLAL  CTRTATGQDC  SAQ....CQC  ...AAEAAPH
nov_chick    .METGGGQGL  PVLLLLLLLL  RPCEVSGREA  ACPRPCGGRC  ..PAEP.PR
ibp_3human   MQRARPTLWA  AALTLLVLLR  GPPVARAGAS  SGGLGPVVRC  EPCVARALAR
ccn-4        ......MK    SVLLTTLLV   PAHLVAAWSN  MYAVDCPQHC  DSSECKSSPR


                51                                                   100
ce10_chick   CAPGVGLVP.  .....DGCGCC  KVCAKQLNED  C....SRTQP  CDHTKGLECN
cyr6_mouse   CAPGVGLVR.  .....DGCGCC  KVCAKQLNED  C....SKTQP  CDHTKGLECN
ctgf_human   CPAGVSLVL.  .....DGCGCC  RVCAKQLGEL  C....TERDP  CDPHKGLFCD
ccn-4        .........   ...........  ..........  ..........  ..........


                401        411
ce10_chick   RLVNDIHKFR  D
cyr6_mouse   SLFNDIHKFR  D
ctgf_human   YYRKMYGDMA  .
fisp-12      YYRKMYGDMA  .
nov_chick    DPMSSEAKI   .
ibp3_human   .........   .
ccn-4        .........   .
```